

Figure 1A

1 AATTGGGCACGAGGGAAATTCAAGCACTTTTCCTAAAAGAAGGGGAATGGATGCTGAAA 60  
61 CAACACGThTCCCACAAAGGGAGCAGACACTGGGCTTGTGAAGCTGCCCCATACCTTCCC 120  
121 CACAGAACTGGGGTCCGGCCTCCCTGACATGCAGATTTCACCCAGAAGACAGAGAAGGA 180  
181 GCCACTGGTCATGGAATGGGCTGGGGTCAAAGACTGGGTGCCTGGGAGCTGAGGCAGCCA 240  
241 CCGTTTCAGCCTGGCCAGCCCTCTGGACCCCGAGGTTGGACCCCTACTGTGACACACCTAC 300  
301 CATGCGGACACTCTTCAACCTCCTCTGGCTTGGCCTGGCCTGCAGCCCTGTTCACTAC 360  
1 M R T L F N L L W L A L A C S P V H T T 20  
361 CCTGTCAAAGTCAGATGCCAAAAAGCCGCTCAAAGACGCTGCTGGAGAAGAGTCAGTT 420  
21 L S K S D A K K A A S K T L L E K S Q F 40  
421 TTCAGATAAGCCGGTGAAGACCGGGGTTTGGTGGTGACGGACCTCAAAGCTGAGAGTGT 480  
41 S D K P V Q D R G L V V T D L K A E S V 60  
481 GGTTCCTGAGCATCGCAGCTACTGCTCGGCAAAGGCCGGGaCAGACACTTTGCTGGGGa 540  
61 V L E H R S Y C S A K A R D R H F A G D 80  
541 TGTACTGGGCTATGTCACTCCATGGAACAGCCATGGCTACGATGTCACCAAGGTCTTTGG 600  
81 V L G Y V T P W N S H G Y D V T K V F G 100  
601 GAGCAAGTTCACACAGATCTCACCCGTCTGGCTGCAGCTGAAGAGACGTGGCCGTGAGAT 660  
101 S K F T Q I S P V W L Q L K R R G R E M 120  
661 GTTTAGGTCACGGCCTCCACGACGTGCACCAAGGGTGGATGCGAGCTGTCAGGAAGCA 720  
121 F E V T G L H D V D Q G W M R A V R K H 140  
721 TGCCAAGGGCCTGCACATAGTGCCTCGGCTCCTGTTGAGGACTGGACTTACGATGATT 780  
141 A K G L H I V P R L L F E D W T Y D D F 160  
781 CCGAACGTCTTAGACAGTGAGGATGAGATAGAGGAGCTGAGCAAGACCGTGGTCCAGGT 840  
161 R N V L D S E D E I E E L S K T V V Q V 180

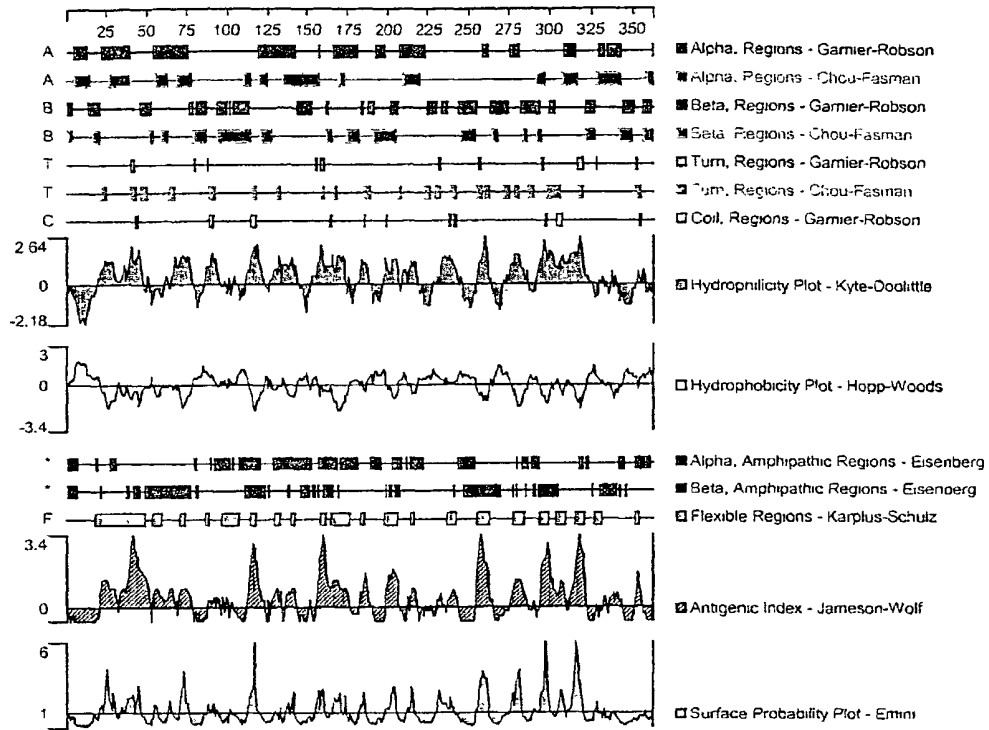
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Figure 1B

841	GGCAAAGAACCAGCATTTCGATGGCTTCGTGGTGGAGGTCTGGAACCAGCTGCTAAGCCA	900
181	A K N Q H F D G F V V E V W N Q L L S Q	200
901	GAAGCGCGTGACCGACCAGCTGGGCATGTTACGCACAAGGAGTTTGAGCAGCTGGCCCC	960
201	K R V T D Q L G M F T H K E F E Q L A P	220
961	CGTGCTGGATGGTTTCAGCCTCATGACCTACGACTACTCTACAGCGCATCAGCCTGGCCC	1020
221	V L D G F S L M T Y D Y S T A H Q P G P	240
1021	TAATGCACCCCTGTCTGGGTTTCGAGCCTGCGTCCAGGTCTGGACCCGAAGTCCAAGTG	1080
241	N A P L S W V R A C V Q V L D P K S K W	260
1081	GCGAAGCAAAATCCTCCTGGGGCTCAACTTCTATGGTATGGACTACGCGACCTCCAAGGA	1140
261	R S X I L L G L N F Y G M D Y A T S K D	280
1141	TGCCCCGTGAGCCTGTTGTGCGGGCCAGGTACATCCAGACACTGAAGGACCACAGGCCCCG	1200
281	A R E P V V G A R Y I Q T L K D H R P R	300
1201	GATGGTGTGGGACAGCCAGGYCTCAGAGCACTTCTTCGAGTACAAGAAGAGCCGCGAGTGG	1260
301	M V W D S Q X S E H F F E Y K K S R S G	320
1261	GAGGCACGTGCTTCTACCCAACCCTGAAGTCCCTGCAGGTGCGGCTGGAGCTGGCCCCG	1320
321	R H V V F Y P T L K S L Q V R L E L A R	340
1321	GGAGCTGGGCGTTGGGGTCTCTATCTGGGAGCTGGGCCAGGGCCTGGACTACTTCTACGA	1380
341	E L G V G V S I W E L G Q G L D Y F Y D	360
1381	CCTGCTCTAGGTGGGCATTGCGGCCTCCGCGGTGGACGTGTTCTTTTCTAAGCCATGGAG	1440
361	L L *	362
1441	TGAGTGAGCAGGTGTGAAATACAGGCCTTCACTCCGTTAAAAAAAAAAAAAAAAAAAAA	1500
1501	AAAAAAAAAAAAAAAAA 1515	

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Figure 2



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Figure 3A

1	GGCAGCAGCCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAACA	60
61	TCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGGATTTCAGGCTCGCCAGCGCCCAGC	120
121	CAGCGAGCCGGCCGGAAGCGCGATGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCC	180
1	M G A P A A S L L L L L L L	13
181	TGCTGTTGCGCTGCTGCTGGGCGCCCGGGGGCCAACTCTCCAGGACGGCTACTGGC	240
14	L F A C C W A P G G A N L S Q D G Y W Q	33
241	AGGAGCAGGATTTGGAGCTGGGAACCTCTGGCTCCACTCGACGAGGCCATCAGCTCCACAG	300
34	E Q D L E L G T L A P L D E A I S S T V	53
301	TCTGGAGCAGCCCTGACATGCTGGCCAGTCAAGACAGCCAGCCCTGGACATCTGATGAAA	360
54	W S S P D M L A S Q D S Q P W T S D E T	73
361	CAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAGTGAAAGATCACGAGGACTCAT	420
74	V V A G G T V V L K C Q V K D H E D S S	93
421	CCCTGCAATGCTTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCCTTC	480
94	L Q W S N P A Q Q T L Y F G E K R A L R	113
481	GAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA	540
114	D N R I Q L V T S T P H E L S I S I S N	133
541	ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAA	600
134	V A L A D E G E Y T C S I F T M P V R T	153
601	CTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTTATA	660
154	A K S L V T V L G I P Q K P I I T G Y K	173
661	AATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCACTCTTCTGGGAGCAAGC	720
174	S S L R E K D T A T L N C Q S S G S K P	193
721	CTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCA	780
194	A A R L T W R K G D Q E L H G E P T R I	213
781	TACAGGAAGATCCCAATGGTAAACCTTCACTGTCAAGCTCGGTGACATTCCAGGTTA	840
214	Q E D P N G K T F T V S S S V T F Q V T	233
841	CCCGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAG	900
234	R E D D G A S I V C S V N H E S L K G A	253

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Figure 3B

901	CTGACAGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGC	960
254	D R S T S Q R I E V L Y T P T A M I R P	273
961	CAGACCTCCCCATCCTCGTGAGGGCCAGAAGCTGTGCTACACTGTGAGGTCGCGGCA	1020
274	D P P H P R E G Q K L L L H C E G R G N	293
1021	ATCCAGTCCCCAGCAGTACCTATGGGAGAAGGAGGCGAGTGTGCCACCCCTGAAGATGA	1080
294	P V P Q Q Y L W E K E G S V P P L K M T	313
1081	CCCAGGAGAGTGGCCTGATCTTCCCTTTCCCTCAACAAGAGTGACAGTGGCACCTACGGCT	1140
314	Q E S A L I F P F L N K S D S G T Y G C	333
1141	GCACAGCCACCAGCAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACC	1200
334	T A T S N M G S Y K A Y Y T L N V N D P	353
1201	CCAGTCCGGTGGCCTCCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTT	1260
354	S P V P S S S S T Y H A I I G G I V A F	373
1261	TCATTGTCTTCTGCTGCTCATCATGCTCATCTTCTCGGCCACTACTTGATCCGGCACA	1320
374	I V F L L L I M L I F L G H Y L I R H K	393
1321	AAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGG	1380
394	G T Y L T H E A K G S D D A P D A D T A	413
1381	CCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCT	1440
414	I I N A E G G Q S G G D D K K E Y F I *	433
1441	AGAGGCGCCTGCCACTTCCTGCGCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTC	1500
1501	ACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCC	1560
1561	ACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGTTTGAATGG	1620
1621	GGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTCCGTTGGCTTCTCTGC	1680
1681	ATTGGGTTATTATTATTTTGTAAACATCCCAAAGCAAATCTGTCTCCAGGCTGGAGAG	1740
1741	GCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAAAAACAAACCCCTGGAGTGTTA	1800
1801	GGAGGAGAGTGAACGTAGAGGGGTGAGGAAGGGTAAGGGGCAGGGCTGGTTTCAGCTGGG	1860

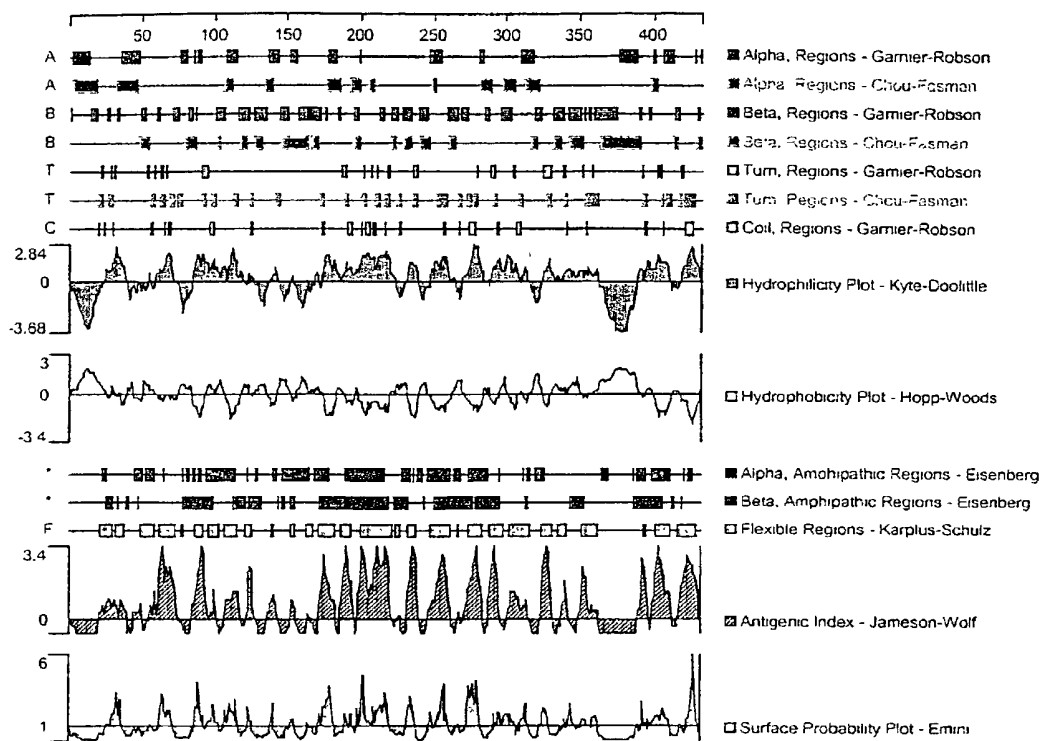
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Figure 3C

1861 GGCTCTCACCAGCCCTCCTTTCAGCCTCTACAACAGAGCAGCTTCCCAGACTTCTCCAGG 1920  
1921 AACCCAGAAACGGGATGGTTGTCTGGCAAAGGTTGGGAGTGGCTTTTCCTCTGGTAGCCAC 1980  
1981 ACACCTGAGCACTACGGACAGGGAGGCAGGTGCCACCTTGACACCTCTCTTCCATAGCAA 2040  
2041 TGGGAAAGTGATGAGTGC GGAGTCTGAGGAGATGTGGCCTGCAGACAACATGCAGCCA 2100  
2101 TGCAGGGACCCAGGACTGTAACTGGGGAGGACGCGGGTCCCTGCAAGGAAGAGTAGATT 2160  
2161 TGGAGAGGAAGGATGGAGGTGGACTCTCACCCCATCCCCCGGAAATGAACAAAGCCGG 2220  
2221 GCCCTTTCCATAGGAACTGCCCTTGAGATAGCAGAGTGTGGCTGCCCCCTCCTTGCTCCA 2280  
2281 GCAGCACTGGGAGAGGCACTGCTCTGGGGCCTGAACTGCTCTGCTTCCCCCCTGAGGG 2340  
2341 GCCCCTCACTCTTACCCAAGACTCTGGATTGTTGCACGGCAACCACTCCTCCCATGGCAT 2400  
2401 TGCTCAGCAACTACTTCTCCCTTCCCGGCCACCCTGTGCCCCCTTCTGGTCCCAACGCC 2460  
2461 AGCCCTTCATCCTTCCTCCCTCAGCAGCCAGGCAGACATAACAACAAACTACTAAAAGG 2520  
2521 AAAAAAAAAAAAAAAAAA 2537

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Figure 4



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Figure 5A

1 CGCCTGGCAC CATGAGGACG CCTGGGGCTC TGCCTGTGCT GCTGCTGCTC CTGGCGGGAG 60  
1 M R T P G P L P V L L L L L A G 16

61 CCCCCGCGGC GGGGCCCCCT CCCCCGACCT GCTACTCCCG CATGCGGGCC CTGAGCCAGG 120  
17 A P A A R P T P P T C Y S R M R A L S Q 36

121 AGATCACC CGACTTCAAC CTCCTGCAGG TCTCGGAGCC CTCGGAGCCA TGTGTGAGAT 180  
37 E I T R D F N L L Q V S E P S E P C V R 56

181 ACCTGCCAG GCTGTACCTG GACATACACA ATTACTGTGT GCTGGACAAG CTGCGGGACT 240  
57 Y L P R L Y L D I H N Y C V L D K L R D 76

241 TTGTGGCCTC GCCCCCGTGT TGAAAGTGG CCCAGGTAGA TTCCTTGAAG GACAAAGCAC 300  
77 F V A S P P C W K V A Q V D S L K D K A 96

301 GGAAGCTGTA CACCATCATG AACTCGTTCT GCAGGAGAGA TTGGGTATTC CTGTGGATG 360  
97 R K L Y T I M N S F C R R D L V F L L D 116

361 ACTGCAATCC CTGGAATAC CCAATCCCAG TGACTACGGT CCTGCCAGAT CGTCAGCGCT 420  
117 D C N A L E Y P I P V T T V L P D R Q R 136

421 AAGGGAAGTG AGACCAGAGA AAGAACCCTA GAGAACTAAA GTTATGTGAG CTACCCAGAC 480

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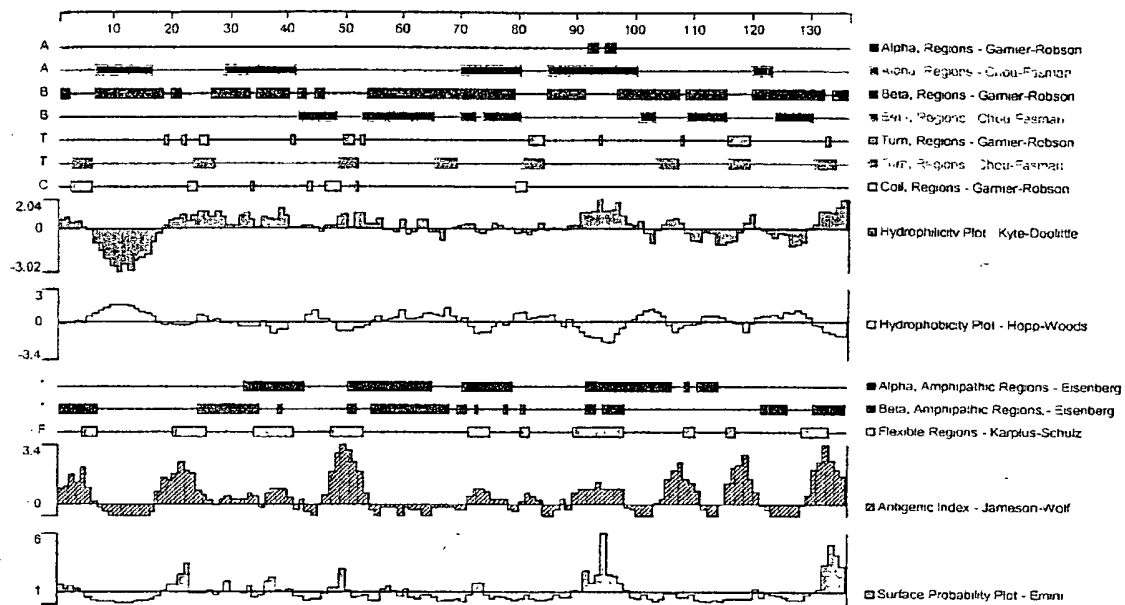


Figure 5B

481 TTAATGGGCC AGAGCCATGA CCTTCACAGG TCTTGTTTA GTTGTATCTG AAACGTGTTAT 540  
541 GTATCTCTCT ACCTTCTGGA AACACGGGCT GGTATTCTTA CCQNGGAACC TCCTTTGAGC 600  
601 ATAGAGTTAG CAACCATGCT TCTCATCCC TTGACTCATG TCTTGCCAGG ATGGTTAGAT 660  
661 ACACAGCATG TTGATTTGGT CACCTAAAAA GAAGAAAAGG ACTAACAAGC TTCACTTTAA 720  
721 TGAACAACIA TTTTGAAC ATGCACAATA GTATGTTTTT ATTACTGGTT TAATGGAGTA 780  
781 ATGGTACTTT TATCTTTTCT TGATAGAAAC CTGCTTACAT TTAACCAAGC TTCTATTATG 840  
841 CCTTTTCTTA ACACAGACTT TCTTCACTGT CTTTCATTTA AAAAGAAATT AATGCTCTTA 900  
901 AGATATATAT TTTAYGTAGT GCTGACAGGA CCCACTCTTT CATTGAAAGG TGATGAAAAT 960  
961 CAAATAAAGA ATCTCTTCAC ATGARAAAAA AAAAAA 996

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Figure 6



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